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(54) Nucleotide sequence coding for an outer membrane protein from Neisseria meningitidis and use

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of said protein in vaccine preparations.

⑤7 The present invention is concerned with a method for the isolation of a nucleotide sequence which codes for a protein having a molecular weight of about 64 000 daltons, which is located on the outer membrane of *N. meningitidis*, as well as with the recombinant DNA obtained therefrom, which is used for the transformation of a host microorganism. The technical object pursued with the invention is the identification of a nucleotide sequence coding for a highly conserved and common protein for the majority of pathogenic *Neisseria* strains, the production of this protein with a high level of purity and in commercially useful amounts using the recombinant way, so that it can be used in diagnostic methods and vaccine preparations with a broad immunoprotection spectrum.

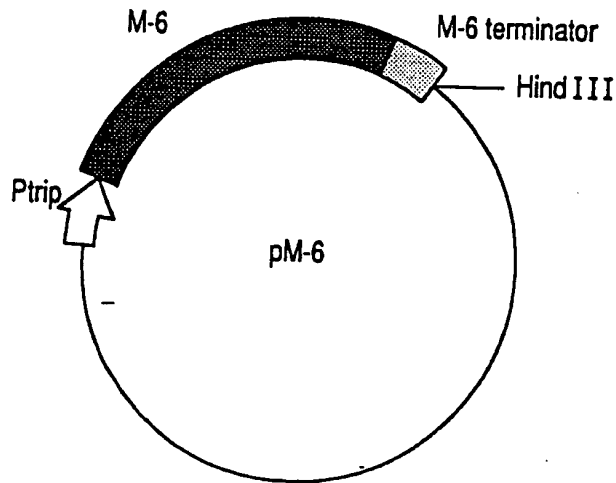


FIG. 1

The present invention is in the field of Genetic Engineering and Biotechnology. More in particular, the invention is related to a nucleotide sequence obtained from the pathogenic bacterium *Neisseria meningitidis*, which nucleotide sequence codes for a protein belonging to the outer membrane of said bacterium. Said protein is cloned and expressed in the host *Escherichia coli*. The characteristics of this protein as well as its capacity to induce immunologically active antibodies (bactericidal antibodies) in its natural host, allow its use in vaccine preparations against pathogenic strains of this microorganism.

The gram-negative bacterium *N. meningitidis* is responsible for one of every three cases of bacterial meningitis in the world. It was described for the first time by Anton Weichselbaum in 1887 (I. DeVoe, 1982, *Microbiol. Revs.* 46: 162-190), and man (i.e. human beings) is its only natural host up to date.

In the first half of this century some essential aspects were found in relation to the metabolism and serological differentiation of this microorganism. The first unsuccessful attempts to obtain vaccine preparations were based on its capsular polysaccharide (E. Kabat et al., 1945, *J. Exp. Med.* 80: 299-307). According to the chemical composition of this capsular polysaccharide, the bacterium *N. meningitidis* is serogrouped in A, B, C, 29-E, H, I, K, L, W-135, X, Y or Z, and the major percentage of illness is caused by A, C, Y, W-135 and B. Non-encapsulated strains are not associated with the invasive disease.

Using different methods of purification of these polysaccharides (E. Gotschlich et al., 1969, *J. Exp. Med.* 129: 1349-1365) the four first polysaccharides (PS) showed to be good immunogens and inducers of bactericidal antibodies in humans (E. Gotschlich et al., 1969, *J. Exp. Med.* 129: 1367-1384). The presence of this kind of antibodies has been correlated previously with non-susceptibility to the infection (I. Goldschneider et al., 1969, *J. Exp. Med.* 129: 1307-1326). As of today mono-, bi- or tetravalent vaccines have been well studied for serotypes A, C and W-135 (F. Ambrosch et al., 1983, *Bulletin of the WHO* 61: 317-323; I. Vodopija et al., 1983, *Infect. Immunol.* 42: 599-604; M. Cadoz et al., 1985, *Vaccine* 3: 340-342; H. Peltola et al., 1985, *Pediatrics* 76: 91-96).

These vaccines have been licensed for their use in humans in different countries (Centers for Disease Control, 1985, *Morbidity and Mortality Weekly Report* 34: 255-259) and some of them are commercially available from different firms and producers (Connaught Laboratories, USA; Smith Kline-RIT, Belgium; Institute Merieux, France; Behringwerke Aktiengesellschaft, Germany; Istituto Sieroterapico e Vaccinazione Toscana "Sclavo", Italy; Swiss Serum and Vaccine Institute, Berne, Switzerland; among others).

However, the conventional vaccine against *N. meningitidis* serogroup C does not induce sufficient levels of bactericidal antibodies in children under 2 years old, which are the principal victims of this disease. It has been demonstrated that the titer of specific antibodies against *N. meningitidis* in children under four years of age, after three years of vaccination, is similar in vaccinated and in non-vaccinated ones (H. Kayhty et al., 1980, *J. of Infect. Dis.* 142: 861-868). Also, no memory response was found against *N. meningitidis* after 8 years of vaccination in young adults (N. Rautonen et al., 1986, *J. of Immunol.* 137: 2670-2675).

The polysaccharide corresponding to *N. meningitidis* serogroup B is poorly immunogenic (E. Gotschlich et al., 1969, *J. Exp. Med.* 129: 1349-1365) and induces a poor response of IgM of low specificity (W. Zollinger et al., 1979, *J. Clin. Invest.* 63: 836-848). There are different theories related to this problem, such as cross-reactivity between B polysaccharide and fetal brain structures, antigenic structures modified in solution and sensitivity to neuroaminidases (C. Moreno et al., 1985, *Infect. Immun.* 47: 527-533). Recently, a chemical modification of PS B was achieved, which induced a response in the host (H. Jennings et al., 1988, *US Patent* 4 727 136; F. Ashton et al., 1989, *Microb. Pathogen.* 6: 455-458), but safety of this vaccine in humans has not been demonstrated.

Due to the lack of an effective vaccine against *N. meningitidis* B, and because the risk of endemic infection is low and mainly restricted to children, a routine immunization with polysaccharides is not recommended (C. Frasch, 1989, *Clin. Microbiol. Revs.* 2: S134-S138) except in the case of an epidemic.

Since after the Second World War the disease was caused in most of the cases by *N. meningitidis* B, vaccines against serogroup B gained special significance.

Other outer membrane components of *N. meningitidis* include phospholipids, lipopolysaccharides (LPS or endotoxins), pili proteins and others. Different immunotypes of LPS have been described for *N. meningitidis* (W. Zollinger and R. Mandrell, 1977, *Infect. Immun.* 18: 424-433; C.M. Tsai et al., 1983, *J. Bacteriol.* 155: 498-504) and immunogenicity using non-toxic derivatives was assayed (H. Jennings et al., 1984, *Infect. Immun.* 43: 407-412) but their variability (H. Schneider et al., 1984, *Infect. Immun.* 45: 544-549) and pyrogenicity (when it is conjugated to lipid A) are limiting factors up to now.

The pili, structures needed to fix cells to nasopharyngeal mucous membrane (D. Stephens et al., 1983, *The J. Infect. Dis.* 148: 369-376) have antigenic diversity among different strains (J. Greenblatt et al., 1988, *Infect. Immun.* 56: 2356-2362) with some common epitopes (D. Stephens et al., 1988, *The J. Infect. Dis.* 158: 332-342). Presently there are some doubts in relation to the effectiveness of a vaccine based on these structures. However some of these types of vaccine have been obtained, without known results related to

their use in humans (C. Brinton, 1988, US Patent 4 769 240).

Recently, the attention has switched to the other proteins of the outer membrane of this bacterium. There are many immunological types of these protein complexes.

The strains of *N. meningitidis* are subdivided in serotypes according to the presence of specific epitopes in the majoritary protein P1/P2 and in subtypes according to other epitopes in protein P1 (C. Frascch et al., 1985, Rev. Infect. Dis. 7: 504-510).

There are several published articles and patent applications concerning vaccines based on cocktails of these proteins, with previous selective removal of endotoxins using biocompatible detergents. The immunogenicity of these cocktails in animals and humans has been demonstrated (W. Zollinger et al., 1979, J. Clin. Invest. 63: 836-848; C. Frascch and M. Peppler, 1982, Infect. Immun. 37: 271-280; E. Beuvery et al., 1983, Infect. Immun. 40: 369-380; E. Rosenqvist et al., 1983, NIPH Annals 6: 139-149; L. Wang and C. Frascch, 1984, Infect. Immun. 46: 408-414; C. Moreno et al., 1985, Infect. Immun. 47: 527-533; E. Wedege and L.

Froholm, 1986, Infect. Immun. 51: 571-578; C. Frascch et al., 1988, The J. Infect. Dis. 158: 710-718; M. Lifely and Z. Wang, 1988, Infect. Immun. 56: 3221-3227; J. Poolman et al., 1988, In J. Poolman et al (Eds), Gonococci and Meningococci, Kluwer Academic Publishers, Dordrecht, The Netherlands, pp 159-165; E. Rosenqvist et al., 1988, J. Clin. Microbiol. 26: 1543-1548), including results in massive field trials e.g. Capetown, South Africa in 1981 (C. Frascch, 1985, Eur. J. Clin. Microbiol. 4: 533-536); Iquique, Chile, 1987 (W. Zollinger, 1988, Proceedings of the Sixth International Pathogenic Neisseria Conference. Callaway Gardens Conference Center) and Cuba 1986 and 1988 (G. Sierra, 1988, Proceedings of the Sixth International Pathogenic Neisseria Conference. Callaway Gardens Conference Center). However, with the exception of the last case, the bactericidal antibodies induced by these preparations were restricted to the same serotype strains or related ones.

One of these vaccines is referred to in US patent 4,601,903 which is restricted to one of the *Neisseria* types producing meningitis (serotype 2), with a high incidence, but also other serotypes have been isolated with high frequency from patients, such as serotypes 4 (Cuba from 1981 to 1983, H. Abdillahi et al., 1988, Eur. J. Clin. Microbiol. Infect. Dis. 7: 293-296; Finland from 1976 to 1987, H. Kayhty et al., 1989, Scand. J. Infect. Dis. 21: 527-535); 8 (Australia from 1971 to 1980, F. Ashton et al., 1984, Can. J. Med. Biol. 30: 1289-1291) and 15 (Norway from 1982 to 1984, L. Froholm et al., 1985, Proceedings of the Fourth International Symposium on Pathogenic Neisseria. American Society for Microbiology; Chile from 1985 to 1987, S. Ruiz et al., 1988, Proceedings of the Sixth International Pathogenic Neisseria Conference. Callaway Gardens Conference Center) as well as strains of undefined serotype (F. Ashton et al., 1980, Can. J. Microbiol. 26: 1480-1488; Australia from 1971 to 1980, F. Ashton et al., 1984, Can. J. Med. Biol. 30: 1289-1291; Finland from 1976 to 1987, H. Kayhty et al., 1989, Scan. J. Infect. Dis. 21: 527-535).

The Cuban vaccine achieved in 1988 by the Centro Nacional de Biopreparados (European Patent Application. No. 301 992) has proven to be very effective. It is based on a high molecular weight antigenic complex. It possesses a broad range of cross-reactivity with other strains and produces and maintains bactericidal antibodies in the immunized host.

However, the methods employed to obtain this type of vaccine start with the multiplication in an appropriate culture of a microorganism which is highly pathogenic, with the associated biological risk of handling directly the bacteria. Moreover, this kind of preparation contains lipopolysaccharides, a contaminant that, although it may increase the product's effectiveness, shows at the same time undesirable secondary effects because of its powerful pyrogenicity. Also, its variation in minor antigenic components, which form part of the preparation, cannot be controlled in the different batches, which makes it difficult to follow important parameters related to the reactogenicity and immunogenicity.

For this reason, there is increasing interest in the identification of nucleotide sequences coding for highly conserved proteins in all strains, and even more so the identification of inducer proteins of bactericidal antibodies common to the majority of pathogenic *Neisseria*, in order to obtain vaccine preparations with a broad spectrum of protection.

There are different proteins with high molecular weight which are present in low amounts in the outer membrane of *N. meningitidis* when this microorganism is grown in conventional culture media but have a strong response in affected individuals (J. Black et al., 1986, Infect. Immun. 54: 710-713; L. Aoun et al., 1988, Ann. Inst. Pasteur/ Microbiol. 139: 203-212) and/or increase their response under special culture conditions (J. van Putten et al., 1987, Antoine van Leeuwenhoek 53: 557-5584; A. Schryvers and L. Morris, 1988, Molecular Microbiol. 2: 281-288 and Infect. Immun. 56: 1144-1149). Some of these proteins are highly conserved among the different strains, in particular those related to the acquisition of iron by the microorganism, that have become interesting vaccine candidates (L. Mocca et al., 1988, Proceedings of the Sixth International Pathogenic Neisseria Conference. Callaway Gardens Conference Center; C. Frascch,

1989, Clin. Microbiol. Revs. 2: S134-S138).

In addition to pure proteins obtained from the micro-organism or strains of related species (e.g. 37 kD protein, T. Mietzner and S. Morse, 1987, US Patent 4 681 761), several related genes have been cloned and expressed. Among these proteins are the following:

- 5 protease IgA1 (J. Koomey and S. Falkow, 1984, Infect. Immun. 43: 101-107);
- protein P1 (A. Barlow et al., 1987, Infect. Immun. 55: 2734-2740, and 1989, Molec. Microbiol. 3: 131-139);
- protein P5a (T. Kawula et al., 1988, Infect. Immun. 56: 380-386);
- protein P5c (T. Olyhoek and M. Achtman, 1988, Proceedings of the Sixth International Pathogenic N. Conference. Callaway Gardens Conference Center);
- 10 protein P4 (K. Klugman et al., 1989, Infect. Immun. 57: 2066-2071);
- protein P2 (K. Murakami et al., 1989, Infect. Immun. 57: 2318-2323);
- and from *N. gonorrhoeae*, which code for proteins with cross-reactivity with their corresponding proteins from *N. meningitidis*:

- antigen H.8 (W. Black and J.G. Cannon, 1985, Infect. Immun. 47: 322-325);
- 15 macromolecular complex (W. Tsai and C. Wilde, 1988, Proceedings of the Sixth International Pathogenic Neisseria Conference. Callaway Gardens Conference Center);
- 37 kDa protein, repressed in the presence of iron (S. Berish et al., 1988, Proceedings of the Sixth International Pathogenic Neisseria Conference. Callaway Gardens Conference Center).

The use of these proteins as active vaccine preparation has not been reported or the bactericidal tests of antibodies induced against them were negative, such as in the case of mouse monoclonal antibodies against H.8 (J. Woods et al., 1987, Infect. Immun. 55: 1927-1928).

Up to the moment, the protein P1 located in the outer membrane of *N. meningitidis* is one of the best characterized and studied antigens. This protein presents no variability within the same strain. However, there are more than 17 types of proteins P1 in *Neisseria* which have differences in three variable regions, this being the basis of the classification of *N.* in different subtypes. This protein is very immunogenic in humans (W.D. Zollinger and R.E. Mandrell, 1983, Med. Trop. 43:143-147), eliciting protective antibodies (E. Wedege and L.O. Froholm, 1986, Infect. Immun. 51: 571-578; K. Saukkonen et al, 1987, Microb. Pathogen. 3:261-267), that give it a special importance in vaccine preparations.

Some subtypes of proteins P1 have been cloned in *E. coli*, starting from genomic libraries (A.K. Barlow et al., 1989, Molec. Microb. 3:131-139) or using the PCR technique (S. Butcher et al., Vllth International Congress of Neisseria, R.C. Seid, Patent Application WO 90/06696; Brian Mc Guinness et al., 1990, J. Exp. Med. 171:1871-1882, M.C.J. Maiden et al., Vllth International Conference of Neisseria, Berlin, Sept. 9-14, 1990, and 1991, Molec. Microb. 3:727; J. Suker et al., Vllth International Conference of Neisseria, Berlin, Sept. 9-14, 1990). However, up to now, there is no genetic construction able to produce this protein with

high levels of expression. Only low levels of expression (D.A. White et al., 1990, Molec. Microb. 4:769:776) or its expression in *Bacillus subtilis* fused to the outer membrane protein A of *E. coli* (omp A) (E. Wahlstrom et al., Vllth International Congress of Neisseria, September 9-14, 1990, Berlin) have been reported.

It can be affirmed that up to the moment no antigen has been isolated which is common to all types and serogroups of *N. meningitidis* and is able to produce bactericidal antibodies. For this reason, an antigen of this kind, conjugated or fused to other proteins or polysaccharides of immunological interest, would be relevant as a candidate for bivalent vaccine preparations.

~~This invention is related to a nucleotide sequence coding for a protein having a molecular weight of about 64 kilodaltons. This sequence has been found in all *N. meningitidis* serotypes and serogroups tested, as verified by nucleic acid hybridization, Western-blotting, Dot-blot and ELISA.~~

45 A technical object of this invention is the identification of a nucleotide sequence which codes for a highly conserved protein and is common to the majority of pathogenic strains of *Neisseria* (named P64k), in order to obtain the protein by a recombinant way with a high grade of purity and in commercially useful quantities, so that it can be employed in diagnostic methods and as an integrating part of a vaccine preparation of broad spectrum of protection.

50 On the level of genetic information (DNA and RNA), the invention provides a recombinant polynucleotide, comprising a nucleotide sequence coding for a protein P64k of *Neisseria meningitidis*, said protein P64k essentially having the amino acid sequence shown in SEQ ID NO:1. In a preferred embodiment said nucleotide sequence coding for the protein P64k of *N. meningitidis* essentially consists of the nucleotide sequence shown in SEQ ID NO:1. The recombinant polynucleotide may further comprise a

55 nucleotide sequence of a cloning or expression vector.

The invention also provides a transformed microorganism containing a recombinant polynucleotide as defined above, preferably a transformed microorganism which is capable of expressing the protein P64k of *N. meningitidis*. In a particularly preferred embodiment of the invention, the transformed microorganism is

an *Escherichia coli* strain, e.g. *E. coli* strain HB101, transformed with an expression vector containing a nucleotide sequence coding for the protein P64k of *N. meningitidis*, e.g. the expression vector pM-6.

The invention also provides a recombinant proteinaceous substance, comprising an amino acid sequence corresponding to the amino acid sequence of at least a part of a protein P64k of *N. meningitidis*, said protein P64k essentially having the amino acid sequence shown in SEQ ID NO:1. Said recombinant proteinaceous substance may essentially consist of protein P64k, or be a fusion protein or a protein/polysaccharide conjugate comprising the amino acid sequence of protein P64k of *N. meningitidis*.

The invention further provides a vaccine composition, comprising a recombinant protein as defined above, together with a suitable carrier, diluent or adjuvant. A particular embodiment of this invention provides a vaccine composition, comprising a lipoamide dehydrogenase or acetyl transferase capable of inducing antibodies which can bind a protein P64k of *N. meningitidis*, together with a suitable carrier, diluent or adjuvant.

In addition, the invention provides a monoclonal antibody, raised against a recombinant proteinaceous substance as defined above, or against a lipoamide dehydrogenase or acetyl transferase, and capable of binding a protein P64k of *N. meningitidis*.

The invention also provides a process for preparing a protein P64k of *Neisseria meningitidis*, or a fusion protein comprising protein P64k, said protein P64k essentially having the amino acid sequence shown in SEQ ID NO:1, comprising the steps of transforming a microorganism with an expression vector containing a nucleotide sequence coding for said protein P64k, or said fusion protein, culturing the transformed microorganism to obtain expression of said protein P64k, or said fusion protein, and isolating said expression product.

One novel aspect of this invention is the gene isolated from the *N. meningitidis* strain B:4:P1.15, which was named M-6 and has as a principal characteristic its stability in *E. coli* vectors. This gene does not produce adverse effects on the host, allowing to obtain yields of over 25 % of total protein (ratio of P64k to total protein from host strain). On the other hand, it has been demonstrated by Southern and Western Blot hybridizations (E. Southern, 1975, *J. Mol. Biol.* 98: 503-527 and W. Burnette, 1981, *Anal. Biochem.* 12: 195-203) that protein P64k is present in all the following studied strains of *N. meningitidis*:

*N. meningitidis* A  
*N. meningitidis* B:1  
*N. meningitidis* B:2  
*N. meningitidis* B:4  
*N. meningitidis* B:5  
*N. meningitidis* B:8  
*N. meningitidis* B:9  
*N. meningitidis* B:11  
*N. meningitidis* B:15  
*N. meningitidis* B:4:P1.15  
*N. meningitidis* C  
*N. meningitidis* B:15:P1.16  
*N. meningitidis* B:15:P1.16 (H 44/76)  
*N. meningitidis* B:NT (121/85)  
*N. meningitidis* B:NT (71/86)  
*N. meningitidis* B:NT (210/86)

and also in *N. mucosa*, *N. subflava* and *N. gonorrhoeae*.

The protein is not present in *N. cinerea*, *N. lactamica*, *N. sicca* and *N. flavescens*, but these are not of interest because they are not pathogenic.

The protein having a molecular weight of about 64 kDa can be localized by electron microscopy in the outer membrane of *N. meningitidis*. Therefore, this antigen is an exposed antigen which is favorable for use in a vaccine preparation. The protein was recognized in Western blot immunoidentification experiments with sera from convalescents and individuals vaccinated with the conventional Cuban vaccine Va-Mengoc-BC (Centro Nacional de Biopreparados, Havana, Cuba). This aspect guarantees the immunogenicity of the antigen and at the same time confirms its presence within the high molecular weight protein fraction constituent of this vaccine, which is responsible of the lasting immune response to the disease.

Another novel aspect is that the protein, which is an object of this invention, produces antibodies with a broad bactericidal spectrum (different serogroups, serotypes and subtypes), a characteristic which has not been reported previously for any protein from *N. meningitidis*.

This protein obtained in high levels in *E. coli* becomes an important candidate for the improvement of immunogenicity when expressed as a fusion protein with other proteins. It could also increase the

expression by conferring enhanced stability and suitability in the molecular structure during transcription and translation processes. Belonging to *Neisseria*, this protein can also be fused to other proteins from *Neisseria* in order to obtain vaccine preparations against this microorganism with increased immunogenicity. These fusion proteins are also objects of this invention.

5 On the other hand, surprisingly, it was found that the gene M-6 obtained from a genomic library of the strain *N. meningitidis* B:4:P1.15 showed a great homology with sequences of lipoamide-dehydrogenases and acetyl-transferases from other microorganisms and higher organisms. The presence of common antigenic determinants allows the use of these other related proteins as immunogens, able to confer protection by the induction of bactericidal antibodies which recognize the antigenic determinants common to protein P64k. Therefore, the use of these lipoamide-dehydrogenases and acetyl-transferases (not isolated from *N. meningitidis*) or derivatives therefrom such as peptides, fragments from enzymatic degradation, constructions of fusion with other proteins, or conjugation with proteins, polysaccharides or lipids, or insertion in complexes as liposomes or vesicles, etc., for vaccine purposes, are included in the scope of this invention.

15 An important object of this invention is the nucleotide sequence which codes for the M-6 gene (SEQ ID NO:1 of the Sequence Listing) whose product is the protein P64k.

This gene was derived from the genome of the strain B385 isolated in Cuba (*N. meningitidis* B:4:P1.15), by the construction of a genomic library in the phage EMBL 3.

The recombinant DNA including the gene M-6 constitutes another object of this invention, which includes the phage lambda, the plasmid pM-3 and the expression vector pM-6 for expression in bacteria.

In particular, for the intracellular expression in *E. coli*, the M-6 gene was cloned under the tryptophane promoter and using its own termination signal of transcription and a linkage fragment between M-6 and the cloning site NcoI which adds the following nucleotide sequence at the 5' end:

ATG CTA GAT AAA AGA (SEQ ID NO:2)

25 The N-terminal of the protein P64k encoded by the M-6 gene inserted in plasmid pM-6 which adds 5 aminoacids to the N-terminal of the original protein corresponds to:

M L D K R M A L V E L K V P D I G G H E N V D I I (SEQ ID NO:3)

Another object of this invention are the microorganisms resulting from the transformation of *E. coli* strain HB 101 with the pM-6 vector, which are characterized by the expression of high levels of protein P64k, good viability and great stability.

30 The transformed clone of *E. coli* was denominated HBM64 (Fig. 2), and presents levels of expression of P64k higher than 25 % in relation to the total protein of the cell (Fig. 6).

The procedure described in the present invention, due to the levels of expression achieved for this product, allows to reach an optimal purity for use of this protein in humans.

35 On the other hand, the antigen obtained from the isolated sequence was very useful in the preparation of different types of potential vaccine preparations, like bivalent vaccines with a broad immunoprotective spectrum, e.g., protein-polysaccharide conjugates, fusion proteins, etc.

EXAMPLES: These examples intend to illustrate the invention, but not to limit the scope of this invention.

#### 40 EXAMPLE 1:

For the isolation of genomic DNA from *N. meningitidis* B:4:P1.15, the cells were grown in Mueller-Hinton medium (OXOID, London). The biomass from a culture of 100 ml was resuspended in 8 ml of Tris (hydroxymethyl-aminomethane) 100 mM, EDTA (ethylenediamine tetraacetic acid) 1mM, pH 8. The cells were subjected to a treatment with lysozyme (10 mg/ml), followed by 200  $\mu$ l of self-digested pronase (20 mg/ml) and 1.1 ml of 10% SDS. The mixture was incubated at 37° C during 1 hour, then it was treated with phenolchloroform (v/v) and the remains of phenol were eliminated using 2-butanol. Finally, the DNA was precipitated with absolute ethanol and RNA was eliminated with ribonuclease A (Sigma, London).

50 The DNA of about 60 kb was subjected to a partial digestion with the enzyme Sau 3A, obtaining a population of fragments of about 15 kb. This majoritary fraction was isolated and purified by separation in agarose gel (T. Maniatis et al., 1982, Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Lab.: Cold Spring Harbor NY).

For the construction of the genomic library, the process described by Maniatis was essentially followed 55 (T. Maniatis et al., 1982, Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Lab.: Cold Spring Harbor NY). Four  $\mu$ g of purified DNA were ligated with 8  $\mu$ g of BamHI-digested EMBL-3. The ligation product was packed and the phages were finally plated on the *E. coli* strain C66P2.

The library was screened by immunoidentification (R. Young and R. Davis, 1983, PNAS USA 80: 1194-

1198) using rabbit serum obtained against a preparation of proteins belonging to the outer membrane of the strain N. meningitidis B:4:P1.15. The clones were analyzed by Western-blot (Burnette, 1981) and the expression of the P64k protein with a molecular weight of about 70 kDa was detected. The resulting recombinant phage was named 31. The Western blot was also made using a mixture of sera from  
 5 convalescents of meningococemia, free of antibodies from E. coli, obtaining the same result as that using hyperimmunized rabbit sera.

This experiment was repeated using sera from several healthy individuals, and the signal obtained was negative against the recombinant protein P64k.

## 10 EXAMPLE 2:

For subcloning in bacteria, the 17 kb insert corresponding to the phage isolated from the library was cloned in the plasmid pUC18 after separation from the phage's arms using the enzyme Sall. This resulted in the construction pM-1 (Fig. 2), that was subjected to restriction analysis (Fig. 3).

15 The fragment Sall-HindIII of about 6 kb was recloned in the plasmid pUC18 and the construction pM-2 was obtained (Fig. 2). In order to obtain a more exact localization of the gene coding for protein P64k deletions were carried out with the enzymes ClaI, EcoRI and HincII. The complete fragment of the gene M-6 was finally localized as an EcoRI-HindIII insert corresponding to the construction pM-3 (Fig. 2).

In all constructions, the presence of the gene was confirmed by recognizing the protein by colony  
 20 immunoidentification and Western Blot using hyperimmunized rabbit sera.

The sequence of the insert in pM-3 was determined by the method of Sanger (F. Sanger et al., 1977, PNAS USA 74: 5463-5467).

From the obtained sequence, the approximate molecular weight of the protein encoded by the gene was deduced.

25 In order to obtain a construction for high expression of the protein P64k, the plasmid pM-3 (Fig. 2) was linearized with the enzyme EcoRI and successive suppressions of the gene were carried out, incubating the sample with the nucleases ExoIII and S1.

The resulting fragments were separated from the rest of the vector pUC18 by cutting with the restriction enzyme HindIII and were cloned fused to a stabilizer fragment (European patent application EP-A-0 416  
 30 673), using an Xba-blunt adapter to conserve the XbaI site of the stabilizer gene:

5' C T A G A T A A A G A 3' (SEQ ID NO:4)

35 3' T A T T T T C T 5' (SEQ ID NO:5)

The constructions in which the fused fragment coincided with the reading frame were selected by  
 40 immunoidentification using hyperimmune rabbit sera.

The insert sequences were established using Sanger's Method (F. Sanger et al., 1977, PNAS USA 74: 5463-5467). From the obtained sequences the approximate molecular weight of the protein encoded by this gene was deduced.

The fusion region between the proteins was localized in the gene sequences. In the clone pILM-25  
 45 (Figure 4) the ATG of the gene predetermined by the sequence of the DNA insert isolated from the library, coincided with the fusion site.

The NcoI-XbaI fragment, corresponding to the stabilizing peptide coding sequence, was deleted from pILM-25, obtaining a non-fused protein expressed under the tryptophan promoter with it's original terminator from the N. Meningitidis B:4:P1.15, according to the pM-6 construction (Figure 1).

50 The pM-6 plasmid was transformed in different strains of E. coli like W3110, JA-221, HB-101, LE-392 and MC-1061, and the expression of P64k was compared. The best results were obtained in W3110, JA-221 and HB-101. These strains were chosen to scale up fermentation, and expression levels up to 25 % of total cell proteins were obtained.

## 55 EXAMPLE 3:

To confirm the correct expression of the cloned gene the N-terminal region of the intact protein was subjected to the Edman degradation method (P. Edman, 1950, Acta Chem. Scand. 4: 283-293). This



technique elucidates the sequence (primary structure) of this region in the molecule.

The P64k protein was desalted by gel filtration chromatography (PD-10, Pharmacia), eluted with water and monitored at 280 nm. The protein fraction was concentrated to 0.5 nM/ $\mu$ l. One  $\mu$ l of this solution was applied to a PVDF (polyvinylidene difluoride, Millipore) filter, previously activated with methanol.

5 The Edman degradation was made using the Knauer's Automatic Sequencer, model 810, connected to a HPLC (High Performance Liquid Chromatography) system, so as to detect the phenylthiohydantoin derivatives of the aminoacids (PTH-aminoacids). The standard procedure of sequencing as recommended by the manufacturer of the equipment was followed. The separation of the PTH-aminoacids was performed in a reverse phase column C-18 (5  $\mu$ m), 250 mm x 2 mm (Merck), eluted with an acetonitrile gradient (B  
10 buffer) in sodium acetate (A buffer), prepared according to the manufacturers, with a 200  $\mu$ l/minute flow and at 42°C. The PTH-aminoacids were detected at 269 nm.

Data processing and registration were made in a Shimadzu model CR-6a automatic integrator, using a program for data processing by subtraction of two consecutive chromatograms, to facilitate the evaluation of the Edman degradation cycles. Sequence identification is obtained by the chromatographic evaluation of the  
15 corresponding analyzed cycle and confirmed by the chromatogram obtained by subtraction, allowing to determine 25 residues.

#### EXAMPLE 4:

20 To demonstrate that the protein P64k is recognized by the sera of individuals vaccinated with the Cuban Va-Mengoc-BC preparation (Centro Nacional de Biopreparados, Havana, Cuba.), a Western-Blot was made, with a mixture of 12 sera from adults (immunized with two doses of the Cuban vaccine) diluted in a solution containing defatted milk (Oxoid, London). The experiment included:  
recombinant protein P64k, purified from E. coli HB-101 transformed with the pM-6 plasmid;  
25 supernatant of the ultrasonic cell rupture of untransformed E. coli HB-101;  
the reaction was revealed with a protein A-colloidal gold conjugate.  
It was shown that the protein P64k is recognized by the pool of sera.

#### EXAMPLE 5:

30 The bactericidal test against B385 (B:4:P1.15) was made according to the procedure described by Larrick et al. (Scand. J. Immunol. 32, 1990, 121-128) with modifications. With this objective, a mixture was made of a) a suspension of bacteria, cultured under special conditions (1-5 colony forming units/1), b) Gey's balanced salt solution, c) rabbit sera (3 to 4 weeks) as a source of complement and d) pooled sera from  
35 mice, immunized against protein P64k in Aluminium Hydroxyde Gel, and inactivated at 56°C for 30 minutes. The immunization of mice was carried out according to an immunization scheme of 3 doses of 20  $\mu$ g each. The proportions used in the aforementioned mixture were 1:2:1:1 in a total volume of 125  $\mu$ l. The mixture was incubated at 37°C during 1 hour and plated in fresh Mueller Hinton Agar (Oxoid, London) supplemented with 5 % calf serum (CubaVet, Habana). The counting of surviving colonies was done after  
40 18 hours of incubation of the plates in an atmosphere of 5 % CO<sub>2</sub> at 37°C.

The bactericidal titer was considered as the maximum serum dilution necessary to render a 50 % inhibition of bacterial growth, with respect to the same mixture without the test serum. It was found that 1:20 serum dilution still maintains its bactericidal activity. As negative controls (non bactericidal at 1:2 dilution) pooled sera from mice immunized with Aluminum Hydroxyde Gel, and pooled sera from mice immunized  
45 with Cuban Hepatitis B recombinant vaccine, were used. The bactericidal effect was specific to the anti-P64k antibodies.

#### EXAMPLE 6:

50 The bactericidal test against different strains of N. meningitidis was made using:  
1. An ammonium sulphate precipitate of the supernatant harvested from a culture of hybridoma cells secreting monoclonal antibodies specific against P64k (anti P64k)/Sample to analyze.  
2. An ammonium sulphate precipitate of the supernatant harvested from hybridoma cells secreting monoclonal antibodies specific against the P1.15 protein present in N. meningitidis strain B385 (anti  
55 P1.15)/Positive control of the system.

The maximum dilutions tested were always 1:16. The maximum dilutions tested which had a bactericidal effect, according to the EXAMPLE 5, are indicated:

Strain	anti-P64k	anti-P1.15
B385	1:16	1:16
B:4:P1.15	1:16	1:16
B:14:P1.7	1:16	-
B:NT:NT	1:16	-
B:15:P1.15	1:8	-
B:15:P1.16	1:8	-
B:13	1:8	-
C	1:16	-
A	1:16	-

As seen, the anti-P64k monoclonal antibodies have significant bactericidal titers against different serogroups (A, B and C), serotypes (4, 14, 13, 15 and NT) and subtypes (7, 15, 16 and NT) of bacteria.

#### EXAMPLE 7:

Fusion protein M-14 (P64k and P1.15)

In order to obtain a genetic construction for high expression that contained the variable epitopes of the P1.15 protein (Outer membrane protein from *N. meningitidis* B:4:P1.15) fused to the P64k protein, the gene coding for P1.15 protein was cloned using the Polymerase Chain Reaction (PCR). The following region containing the variable immunodeterminants of P1.15:

```

L Q L T E P P S K S Q P Q V K V T K A K S R I R T K I S D F G
S F I G F K G S E D L G E G L K A V W Q L E Q D V S V A G G G
A T Q W G N R E S F V G L A G E F G T L R A G R V A N Q F D D
A S Q A I D P W D S N N D V A S Q L G I F K R H D D M P V S V
R Y D S P D F S G F S G S V Q F V P I Q N S K S A Y T P A Y H
Y T R Q N N A D V F V P A V V G K P G S D V Y V A G L N Y K N
G G F A G S Y A F K Y A R H A N V G R N A F E L F L L G S T S
D E A

```

(SEQ ID NO:6)

was inserted in the Mlu I site of the gene M-6, encoding for P64k, after having been made blunt with the klenow fragment from DNA polymerase I. The sites for gene fusion of P1.15 with M-6 are the following:

```

GDALQL

```

(SEQ ID NO:7)

45

```

      Gly Asp Ala  Leu Gln Leu
5'-  GGC GAC GCG  CTG CAG TTGA  -3'  (SEQ ID NO:8)
      M-6                P1.15

```

55

EANAYE

(SEQ ID NO:9)

5

Glu Ala Asn\*Ala Tyr Glu

5'- GAA GCC AAC GCG TAC GAA -3' (SEQ ID NO:10)

P1.15

M-6

10

\*: N does not belong to any of the fusion proteins and was created by the genetic construction.

15

The resulting fusion protein (M-14) was expressed in *E. coli* using a plasmid vector under the tryptophan promoter, to levels higher than 10 % of total cell protein. The protein was recognized by bactericidal monoclonal antibodies, and anti-P1.15 and P64k polyclonal antibodies, in Western-Blot.

## 20 EXAMPLE 8:

Polysaccharide/P64k conjugation.

The protein P64k was conjugated with the polysaccharide from *Haemophilus influenzae* using the reductive amination method. The *Haemophilus influenzae* polysaccharide (Polyribosyl ribitol phosphate, PRP) was purified by the cold phenol method described by Frasch, 1990 (in: *Bacterial Vaccines*, 1990, Alan R. Liss, Inc., pp. 123-145). The final contamination of PRP with proteins or nucleic acids was less than 1 %. This polysaccharide was degraded using the method of Parikh et al. 1974 (*Methods in Enzymol.* 34B: 77-102) with sodium periodate in PRP (ratio 1 : 5 w/w) dissolved in 0.1 M sodium acetate (pH 4.5). The incubation was carried out in the dark during 30 minutes with stirring. The periodate excess was eliminated by addition of ribitol. Very low molecular weight compounds were eliminated by dialysis (Medicell International Ltd. Membrane, London). The resulting oligosaccharide had free aldehyde groups able to react with primary amines (e.g. lysine residues in proteins). The conjugate is obtained by mixing protein and polysaccharide in a 1 : 1 ratio (w/w), adding sodium cyanoborohydride and subjecting the mixture to an incubation, first for 48 hours at 4°C and later at 37°C for 24 hours. The high molecular weight complex which contains the resulting conjugate with protein-polysaccharide in a 1 : 2.3 ratio, can be separated from the non reactive contaminants by HPLC.

## EXAMPLE 9:

40

Bivalent vaccine preparation against Hepatitis B virus and *N. meningitidis*.

In order to obtain a bivalent vaccine preparation, different quantities of protein P64k and Hepatitis B Surface Antigen (Vacuna Recombinante contra 1a Hepatitis B, Heber Biotec, Havana, Cuba) were mixed. The antigens were adjuvated with Aluminum Hydroxyde Gel, at 2mg/dose and inoculated in Balb/c mice having a body weight of 20 g in 3 dosis of 0.5 ml each. Different variants were assayed:

1. P64k 20 µg (P20)
2. HBsAg 20 µg (H20)
3. P64k 10 µg + HBsAg 10 µg (P10:H10)
4. P64K 15 µg + HBsAg 5 µg (P15:H5)
5. Placebo (Al(OH)<sub>3</sub>)

50

Seven days after the immunization with the first doses, the second doses were applied. The third dose was given 14 days after the second. Seven days later, blood was taken and the serum of each immunized animal was separated. Antibody titers against P64k protein were measured in solid phase Enzyme Linked Immunosorbent Assay (ELISA), using P64k at 5 mg/ml to coat the polystyrene plate. The antibody titers against HBsAg were determined by a Commercial ELISA (Organon Teknika, Baxtel). Figure 5 shows the dynamics of antibody response against protein P64k, using sera diluted 1/10 000. The response against P64k is not interfered by the presence of the other antigen. Figure 6 shows the titers against HBsAg after each dosis. The titers against this protein are not diminished by the presence of P64k in the preparation.

55

High titers are obtained against both antigens in the same vaccine preparation.

# EXAMPLE 10:

5 A software was created to search the EMBL (European Molecular Biology Laboratory) Data Base and detect the homology between P64k and other proteins. As result of the search it was found that there is homology of one segment in the sequence of P64k with segments in the sequences of *N. gonorrhoeae*. This sequence was found as characteristic in both *N. gonorrhoeae* and *N. meningitidis* (F.F. Correia, S. Inouye and M. Inouye, 1988, J. Biol. Chem. 263, No. 25, 12194-12198).

10 Another region with high homology was found in two proteins of the Pyruvate Dehydrogenase Complex from *E. coli* K12:

a) Acetyltransferase from *E. coli* and the P64k outer membrane protein from *N. meningitidis*.

15 Homology exists between a segment comprising 100 amino acids, repeated at the beginning of the amino acid sequence of the Acetyltransferase ("Lipoyl Domain", including the "Lipoyl Binding Site" (P.E. Stephens et al., 1983, Eur. J. Biochem. 133, 481-489)) and a region located in the first 111 amino acids of the P64k:

20	MALVELKVPDIGGHENVDIIAVEVNVGDTIAV	(SEQ ID NO:11)
	- * - * * * * * - * - * * * * *	
	VKEVNVDPDIGG DEVEVTEVMVKVGDKVAA	(SEQ ID NO:12)
25	DDTLITLETDKATMDVPAEVAGVVKEVKVKVG	(SEQ ID NO:11) (cont)
	-- * * * - * * * * - * * * * * * * * * * * *	
	EQSLITVEGDKASMEVPAPFAGVVKELKVNVG	(SEQ ID NO:12) (cont)
30	DKISEGGLIVVVEAEGT--AAPKAESAA--A	(SEQ ID NO:11) (cont)
	* * - * * * - * * * * * * * - * * *	
	DKVKTGSLIMIFEVEGAAPAAAPAKQEAAAPA	(SEQ ID NO:12) (cont)
35	PRKKPLKCRWVPQAAQFGG	(SEQ ID NO:11) (cont)
	* * * * * * *	
	PAAKAEAPAAAPAAKAEGK	(SEQ ID NO:12) (cont)

40 where (\*) indicates positions with the same amino acids and (-) indicates positions of conservative amino acid changes.

b) Lipoamide Dehydrogenase from *E. coli* and Outer Membrane P64k protein from *N. meningitidis*.

45 Homology exists between the Lipoamide Dehydrogenase from *E. coli* (a protein having 473 amino acids, P.E. Stephens et al., 1983, Eur. J. Biochem. 133, 481-489) and the protein P64k, specifically in a segment which represents almost the total protein, except the region with homology with the "lipoyl domain" from Acetyltransferase.

50

55

	---1---	
	SADAEYDVVVLGGPGGYSAAFAAADEGLKVA	(SEQ ID NO:13)
5	*-- - *****--*----- ** *--	
	STEIKTQVVVLGAGPAGYSAAFRCADLGLETV	(SEQ ID NO:14)
	-----2-----	
10	IVERYKTLGGVCLNVGCIPSKALLHNAVIDE	(SEQ ID NO:13) (cont)
	*****-----*-----*-----*	
	IVERYNTLGGVCLNVGCIPSKALLHVAKVIEE	(SEQ ID NO:14) (cont)
15	VRHLAANGIKYPEPALDIDMLRAYKDGVSRL	(SEQ ID NO:13) (cont)
	-- **--*--*--*--*--*--*--*--*	
	AKALAEHGIVFGEPKTDIDKI TWKEKVINQL	(SEQ ID NO:14) (cont)
20	TG-FGRYGEKRKVDVIQGDGQFLDPHHLEVSL	(SEQ ID NO:13) (cont)
	** -- -- *--*--*--*--*--*--*	
	TGGLAGMAKGRKV̄VVNGLGKFTGANTLEVEG	(SEQ ID NO:14) (cont)
25	TAGDAYEQAAPTGEKKIVAFKNCIIAAGSRVT	(SEQ ID NO:13) (cont)
	--* *-----*-----*-----*	
	ENG-----KTVINFDNAIIAAGSRPI	(SEQ ID NO:14) (cont)
30	KLPFIP-EDPRIIDSSGALALKEVPGKLLIIG	(SEQ ID NO:13) (cont)
	***** *-----*-----*-----*	
	QLPFIPHEDPRIWDSTDALELKEVPERLLVMG	(SEQ ID NO:14) (cont)
35	GGIIGLEMGTVYSTLGSRLDVVEMMDGLMQGA	(SEQ ID NO:13) (cont)
	***** *-----*-----*-----*	
	GGIIGLEMGTVYHALGSQIDVVEMFDQVIPAA	(SEQ ID NO:14) (cont)
40	DRDLVKVWQKQNEYRFDNIMVNTKTVAVEPKE	(SEQ ID NO:13) (cont)
	*--*--*--*--*--*--*--*--*--*	
	DKDIVKVFTKRISKKN-LMLETKVTAVEAKE	(SEQ ID NO:14) (cont)
45	DGVYVTFEGANPPKEPQRYDAVLVAAGRPNP	(SEQ ID NO:13) (cont)
	**--*--*--*--*--*--*--*--*--*	
	DGIYVTMEGKKAPAEPQRYDAVLVAIGRVPNG	(SEQ ID NO:14) (cont)
50	KLISAEKAGVAVTDRGFIEVDKQMRNTNPHIY	(SEQ ID NO:13) (cont)
	* --*--*--*--*--*--*--*--*--*	
	KNLDAGKAGVEVDDRGFIRVDKQLRTNPHIF	(SEQ ID NO:14) (cont)

55

AIGDIVGQPM LAHKAVHEGHVAAENCAGTKAY (SEQ ID NO:13) (cont)  
 \*\*\*\*\*  
 AIGDIVGQPM LAHKGVHEGHVAAEVIAGKKHY (SEQ ID NO:14) (cont)  
 5  
 FDAVIPGVAYTSPEVAWVGETELSAKRPAGK (SEQ ID NO:13) (cont)  
 \*\*\_ \*\*\*\_\*\*\*\_\*\*\*\_\*\*\*\_\*\*\*\_\*\*\*\_\*\*\_\*\*\*\_\*\*\_\*\*  
 FDPKVIPSIAYTEPEVAWVGLTEKEAKEKGIS (SEQ ID NO:14) (cont)  
 10  
 ITKANFPWAASGRAIANGCDKPF TKLIFDAET (SEQ ID NO:13) (cont)  
 \*-\*-\*-\*-\*-\*-\*-\*-\*-\*-\*-\*-\*-\*-\*-\*-\*-\*-\*-\*  
 YETATFPWAASGRAIASDCADGMTKLIFDKES (SEQ ID NO:14) (cont)  
 15  
 GRIIGGGIVGPNGGDMIAKSALPSKLGCAAD (SEQ ID NO:13) (cont)  
 \*-\*-\*-\*-\*-\*-\*-\*-\*-\*-\*-\*-\*-\*-\*-\*-\*-\*-\*-\*  
 HRVIGGAIVGTNGGELLGEIGLAIEMGCAED (SEQ ID NO:14) (cont)  
 20  
 |--3-|  
 VGKTIHPRPTLGESIGMAAEVALGTCTDLPPQ (SEQ ID NO:13) (cont)  
 -- \*\*\*\_\*\*\*\_\*\*\*\_\*\*\*\_\*\*\*\_\*\*\*\_\*\*\_\*\*\*\_\*\*\_\*\*  
 25 IALTIHAHPTLHESVGLAAEVFEGSITDLPNP (SEQ ID NO:14) (cont)  
 --KKK - MEN1pd (SEQ ID NO:13) (cont)  
 \*\*\*  
 30 KAKKK - EC1pd (SEQ ID NO:14) (cont)

## Where:

- 35 |-1-|: Adenine binding site (FAD)  
 |-2-|: Redox active disulphide region  
 |-3-|: Active site histidine

## Strain deposits:

- 40 An E. coli HB-101 clone containing the plasmid pM-3 (a pUC18 plasmid containing the 4.1 kb DNA fragment from *Neisseria meningitidis*, strain B:4:P1.15, cloned between the EcoRI and HindIII restriction sites), was deposited on August 30, 1991, with the Centraalbureau voor Schimmelcultures (CBS), Baarn, The Netherlands, and obtained deposit number CBS 485 .91.

45

50

55

## SEQUENCE LISTING

5

SEQ ID NO:1

SEQUENCE TYPE : Nucleotide with corresponding amino acid

10

SEQUENCE LENGTH: 1830 bp

STRANDEDNESS: Single

TOPOLOGY: Linear

15

MOLECULE TYPE: genomic DNA

ORIGINAL SOURCE ORGANISM: N. meningitidis group B

IMMEDIATE EXPERIMENTAL SOURCE: Strain B:4:P1:15 isolated in  
Cuba

20

FEATURES: From-1 to 1830 bp mature protein

PROPERTIES: Gene coding for P64k protein from outer membrane  
of N. meningitidis

25

ATG	CTA	GAT	AAA	AGA	ATG	GCT	TTA	GTT	GAA	TTG	AAA	GTG	CCC	42
Met	Leu	Asp	Lys	Arg	Met	Ala	Leu	Val	Glu	Leu	Lys	Val	Pro	
1				5					10					

30

GAC	ATT	GGC	GGA	CAC	GAA	AAT	GTA	GAT	ATT	ATC	GCG	GTT	GAA	84
Asp	Ile	Gly	Gly	His	Glu	Asn	Val	Asp	Ile	Ile	Ala	Val	Glu	
15				20					25					

35

GTA	AAC	GTG	GGC	GAC	ACT	ATT	GCT	GTG	GAC	GAT	ACC	CTG	ATT	126
Val	Asn	Val	Gly	Asp	Thr	Ile	Ala	Val	Asp	Asp	Thr	Leu	Ile	
30				35					40					

40

ACT	TTG	GAA	ACC	GAT	AAA	GCG	ACT	ATG	GAC	GTA	CCT	GCT	GAA	168
Thr	Leu	Glu	Thr	Asp	Lys	Ala	Thr	Met	Asp	Val	Pro	Ala	Glu	
45				50					55					

45

GTT	GCA	GGC	GTA	GTC	AAA	GAA	GTT	AAA	GTT	AAA	GTC	GGC	GAC	210
Val	Ala	Gly	Val	Val	Lys	Glu	Val	Lys	Val	Lys	Val	Gly	Asp	
			60					65				70		

AAA	ATC	TCT	GAA	GGT	GGT	TTG	ATT	GTC	GTC	GTT	GAA	GCT	GAA	252
Lys	Ile	Ser	Glu	Gly	Gly	Leu	Ile	Val	Val	Val	Glu	Ala	Glu	
				75				80						

50

GGC	ACG	GCA	GCC	GCT	CCT	AAA	GCC	GAA	TCG	GCT	GCC	GCC	CCG	294
Gly	Thr	Ala	Ala	Ala	Pro	Lys	Ala	Glu	Ser	Ala	Ala	Ala	Pro	
85				90				95						

55

	CGC	AAG	AAG	CCC	CTA	AAC	GTG	CCG	CTC	CCT	GCT	CCG	CAA	GCC	336
	Arg	Lys	Lys	Pro	Leu	Asn	Val	Pro	Leu	Pro	Ala	Pro	Gln	Ala	
	100						105					110			
5	GCG	CAA	TTC	GGC	GGT	TCT	GCC	GAT	GCC	GAG	TAC	GAT	GTG	GTC	378
	Ala	Gln	Phe	Gly	Gly	Ser	Ala	Asp	Ala	Glu	Tyr	Asp	Val	Val	
	115						120					125			
10	GTA	TTG	GGT	GGC	GGT	CCC	GGC	GGT	TAC	TCC	GCT	GCA	TTT	GCC	420
	Val	Leu	Gly	Gly	Gly	Pro	Gly	Gly	Tyr	Ser	Ala	Ala	Phe	Ala	
				130					135					140	
15	GCT	GCC	GAT	GAA	GGC	TTG	AAA	GTC	GCC	ATC	GTC	GAA	CGT	TAC	462
	Ala	Ala	Asp	Glu	Gly	Leu	Lys	Val	Ala	Ile	Val	Glu	Arg	Tyr	
					145					150					
20	AAA	ACT	TTG	GGC	GGC	GTT	TGC	CTG	AAC	GTC	GGC	TGT	ATC	CCT	504
	Lys	Thr	Leu	Gly	Gly	Val	Cys	Leu	Asn	Val	Gly	Cys	Ile	Pro	
	155					160					165				
25	TCC	AAA	GCC	TTG	TTG	CAC	AAT	GCC	GCC	GTT	ATC	GAC	GAA	GTG	546
	Ser	Lys	Ala	Leu	Leu	His	Asn	Ala	Ala	Val	Ile	Asp	Glu	Val	
	170						175					180			
30	CGC	CAC	TTG	GCT	GCC	AAC	GGT	ATC	AAA	TAC	CCC	GAG	CCG	GAA	588
	Arg	His	Leu	Ala	Ala	Asn	Gly	Ile	Lys	Tyr	Pro	Glu	Pro	Glu	
			185					190					195		
35	CTC	GAC	ATC	GAT	ATG	CTT	CGC	GCC	TAC	AAA	GAC	GGC	GTA	GTT	630
	Leu	Asp	Ile	Asp	Met	Leu	Arg	Ala	Tyr	Lys	Asp	Gly	Val	Val	
				200					205					210	
40	TCC	CGC	CTC	ACG	GGC	GGT	TTG	GCA	GGT	ATG	GCG	AAA	AGC	CGT	672
	Ser	Arg	Leu	Thr	Gly	Gly	Leu	Ala	Gly	Met	Ala	Lys	Ser	Arg	
					215					220					
45	AAA	GTG	GAC	GTT	ATC	CAA	GGC	GAC	GGG	CAA	TTC	TTA	GAT	CCG	714
	Lys	Val	Asp	Val	Ile	Gln	Gly	Asp	Gly	Gln	Phe	Leu	Asp	Pro	
	225					230					235				
50	CAC	CAC	TTG	GAA	GTG	TCG	CTG	ACT	GCC	GGC	GAC	GCG	TAC	GAA	756
	His	His	Leu	Glu	Val	Ser	Leu	Thr	Ala	Gly	Asp	Ala	Tyr	Glu	
	240						245					250			
55	CAG	GCA	GCC	CCT	ACC	GGC	GAG	AAA	AAA	ATC	GTT	GCC	TTC	AAA	798
	Gln	Ala	Ala	Pro	Thr	Gly	Glu	Lys	Lys	Ile	Val	Ala	Phe	Lys	
			255					260					265		
60	AAC	TGT	ATC	ATT	GCA	GCA	GGC	AGC	CGC	GTA	ACC	AAA	CTG	CCT	840
	Asn	Cys	Ile	Ile	Ala	Ala	Gly	Ser	Arg	Val	Thr	Lys	Leu	Pro	
				270					275					280	



	TTC	ATT	CCT	GAA	GAT	CCG	CGC	ATC	ATC	GAT	TCC	AGC	GGC	GCA	882
	Phe	Ile	Pro	Glu	Asp	Pro	Arg	Ile	Ile	Asp	Ser	Ser	Gly	Ala	
				285						290					
5	TTG	GCT	CTG	AAA	GAA	GTA	CCG	GGC	AAA	CTG	CTG	ATT	ATC	GGC	924
	Leu	Ala	Leu	Lys	Glu	Val	Pro	Gly	Lys	Leu	Leu	Ile	Ile	Gly	
	295					300					305				
10	GGC	GGC	ATT	ATC	GGC	CTC	GAG	ATG	GGT	ACG	GTT	TAC	AGC	ACG	966
	Gly	Gly	Ile	Ile	Gly	Leu	Glu	Met	Gly	Thr	Val	Tyr	Ser	Thr	
		310					315					320			
15	CTG	GGT	TCG	CGT	TTG	GAT	GTG	GTT	GAA	ATG	ATG	GAC	GGC	CTG	1008
	Leu	Gly	Ser	Arg	Leu	Asp	Val	Val	Glu	Met	Met	Asp	Gly	Leu	
			325					330					335		
20	ATG	CAA	GGC	GCA	GAC	CGC	GAT	TTG	GTA	AAA	GTA	TGG	CAA	AAA	1050
	Met	Gln	Gly	Ala	Asp	Arg	Asp	Leu	Val	Lys	Val	Trp	Gln	Lys	
				340					345					350	
	CAA	AAC	GAA	TAC	CGT	TTT	GAC	AAC	ATT	ATG	GTC	AAC	ACC	AAA	1092
	Gln	Asn	Glu	Tyr	Arg	Phe	Asp	Asn	Ile	Met	Val	Asn	Thr	Lys	
					355					360					
25	ACC	GTT	GCA	GTT	GAG	CCG	AAA	GAA	GAC	GGC	GTT	TAC	GTT	ACC	1134
	Thr	Val	Ala	Val	Glu	Pro	Lys	Glu	Asp	Gly	Val	Tyr	Val	Thr	
	365					370					375				
30	TTT	GAA	GGC	GCG	AAC	GCC	CCT	AAA	GAG	CCG	CAA	CGC	TAC	GAT	1176
	Phe	Glu	Gly	Ala	Asn	Ala	Pro	Lys	Glu	Pro	Gln	Arg	Tyr	Asp	
		380					385					390			
35	GCC	GTA	TTG	GTT	GCC	GCC	GGC	CGC	GCG	CCC	AAC	GGC	AAA	CTC	1218
	Ala	Val	Leu	Val	Ala	Ala	Gly	Arg	Ala	Pro	Asn	Gly	Lys	Leu	
			395					400					405		
40	ATC	AGC	GCG	GAA	AAA	GCA	GGC	GTT	GCC	GTA	ACC	GAT	CGC	GGC	1260
	Ile	Ser	Ala	Glu	Lys	Ala	Gly	Val	Ala	Val	Thr	Asp	Arg	Gly	
				410					415					420	
45	TTC	ATC	GAA	GTG	GAC	AAA	CAA	ATG	CGT	ACC	AAT	GTG	CCG	CAC	1302
	Phe	Ile	Glu	Val	Asp	Lys	Gln	Met	Arg	Thr	Asn	Val	Pro	His	
					425					430					
50	ATC	TAC	GCC	ATC	GGC	GAC	ATC	GTC	GGT	CAG	CCG	ATG	TTG	GCG	1344
	Ile	Tyr	Ala	Ile	Gly	Asp	Ile	Val	Gly	Gln	Pro	Met	Leu	Ala	
	435					440					445				
55	CAC	AAA	GCC	GTT	CAC	GAA	GGC	CAC	GTT	GCC	GCC	GAA	AAC	TGC	1386
	His	Lys	Ala	Val	His	Glu	Gly	His	Val	Ala	Ala	Glu	Asn	Cys	
		450					455					460			

GCC GGC AAC AAA GCC TAC TTC GAC GCA CGG GTG ATT CCG GGC 1428  
 Ala Gly Asn Lys Ala Tyr Phe Asp Ala Arg Val Ile Pro Gly  
 465 470 475

5 GTT GCC TAC ACT TCC CCC GAA GTG GCG TGG GTG GGC GAA ACC 1470  
 Val Ala Tyr Thr Ser Pro Glu Val Ala Trp Val Gly Glu Thr  
 480 485 490

10 GAA CTG TCC GCC AAA GCC TCC GCG CGC AAA ATC ACC AAA GCC 1512  
 Glu Leu Ser Ala Lys Ala Ser Ala Arg Lys Ile Thr Lys Ala  
 495 500

15 AAC TTC CCG TGG GCG GCT TCC GGC CGT GCG ATT GCC AAC GGT 1554  
 Asn Phe Pro Trp Ala Ala Ser Gly Arg Ala Ile Ala Asn Gly  
 505 510 515

20 TGC GAC AAG CCG TTT ACC AAG CTG ATT TTT GAT GCC GAA ACC 1596  
 Cys Asp Lys Pro Phe Thr Lys Leu Ile Phe Asp Ala Glu Thr  
 520 525 530

25 GGC CGC ATC ATC GGC GGC GGC ATT GTC GGT CCG AAC GGT GGC 1638  
 Gly Arg Ile Ile Gly Gly Gly Ile Val Gly Pro Asn Gly Gly  
 535 540 545

GAT ATG ATC GCG AAG TCT GCC TTG CCA TCG AAA TGG GCT GCG 1680  
 Asp Met Ile Ala Lys Ser Ala Leu Pro Ser Lys Trp Ala Ala  
 550 555 560

30 ACA CGT GCA GAC ATC GGC AAA ACC ATC CAC CCG CGC CCG ACC 1722  
 Thr Arg Ala Asp Ile Gly Lys Thr Ile His Pro Arg Pro Thr  
 565 570

35 TTG GGC GAA TCC ATC GGT ATG GCG GCG GAA GTG GCA TTG GGT 1764  
 Leu Gly Glu Ser Ile Gly Met Ala Ala Glu Val Ala Leu Gly  
 575 580 585

40 ACT TGT ACC GAC CTG CCT CCG CAA AAG AAA AAA TAA 1800  
 Thr Cys Thr Asp Leu Pro Pro Gln Lys Lys Lys \*  
 590 595 599

ATCC GACTGAATAA ACAGCCGATA AGGT TTATTT GA 1836

45 SEQ ID NO: 2  
 SEQUENCE TYPE : Nucleotide  
 SEQUENCE LENGTH: 15 bases

50 ATGCTAGATA AAAGA 15

55

SEQ ID NO: 3

SEQUENCE TYPE : Amino acid

SEQUENCE LENGTH: 25 amino acids

MOLECULE TYPE: Sequence N-terminal of P64k protein from outer  
membrane of N. meningitidis

Met	Leu	Asp	Lys	Arg	Met	Ala	Leu	Val	Glu	Leu	Lys	Val	Pro	Asp
1				5					10					15
Ile	Gly	Gly	His	Glu	Asn	Val	Asp	Ile	Ile					
				20					25					

SEQ ID NO: 4

SEQUENCE TYPE : Nucleotide

SEQUENCE LENGTH: 12 bases

CTAGATAAAA GA 12

SEQ ID NO: 5

SEQUENCE TYPE : Nucleotide

SEQUENCE LENGTH: 8 bases

TCTTTTAT 8

SEQ ID NO: 6

SEQUENCE TYPE : Amino acid

SEQUENCE LENGTH: 221 amino acids

MOLECULE TYPE: Sequence which includes variable regions of  
P1.15 protein

Leu	Gln	Leu	Thr	Glu	Pro	Pro	Ser	Lys	Ser	Gln	Pro	Gln	Val	Lys
1				5					10					15
Val	Thr	Lys	Ala	Lys	Ser	Arg	Ile	Arg	Thr	Gln	Ile	Ser	Asp	Phe
				20					25					30
Gly	Ser	Phe	Ile	Gly	Phe	Lys	Gly	Ser	Glu	Asp	Leu	Gly	Glu	Gly
				35					40					45
Leu	Lys	Ala	Val	Trp	Gln	Leu	Glu	Gln	Asp	Val	Ser	Val	Ala	Gly
				50					55					60

Gly Gly Ala Thr Gln Trp Gly Asn Arg Glu Ser Phe Val Gly Leu  
 65 70 75  
 5  
 Ala Gly Glu Phe Gly Thr Leu Arg Ala Gly Arg Val Ala Asn Gln  
 80 85 90  
 Phe Asp Asp Ala Ser Gln Ala Ile Asp Pro Trp Asp Ser Asn Asn  
 10 95 100 105  
 Asp Val Ala Ala Ser Gln Leu Gly Ile Phe Lys Arg His Asp Asp  
 110 115 120  
 15 Met Pro Val Ser Val Arg Tyr Asp Ser Pro Asp Phe Ser Gly Phe  
 125 130 135  
 Ser Gly Ser Val Gln Phe Val Pro Ile Gln Asn Ser Lys Ser Ala  
 140 145 150  
 20 Tyr Thr Pro Ala Tyr His Tyr Thr Arg Gln Asn Asn Ala Asp Val  
 155 160 165  
 Phe Val Pro Ala Val Val Gly Lys Pro Gly Ser Asp Val Tyr Val  
 25 170 175 180  
 Ala Gly Leu Asn Tyr Lys Asn Gly Gly Phe Ala Gly Ser Tyr Ala  
 185 190 195  
 30 Phe Lys Tyr Ala Arg His Ala Asn Val Gly Arg Asn Ala Phe Glu  
 200 205 210  
 Leu Phe Leu Leu Gly Ser Thr Ser Asp Glu Ala  
 215 220  
 35

SEQ ID NO: 7

SEQUENCE TYPE : Amino acid

40 SEQUENCE LENGTH: 6 amino acids

MOLECULE TYPE: Sequence corresponding to the fusion site  
 between N-terminal of P64k and P1.15

45 Gly Asp Ala Leu Gln Leu  
 1 5

50

55

SEQ ID NO: 8

SEQUENCE TYPE : Nucleotide

SEQUENCE LENGTH: 19 bases

MOLECULE TYPE: Sequence corresponding to the fusion of  
N-terminal from gene M-6 and from gene P1.15

GGCGACGCGC TGCAGTTGA

19

SEQ ID NO: 9

SEQUENCE TYPE : Amino acid

SEQUENCE LENGTH: 6 amino acids

MOLECULE TYPE: Sequence corresponding to the fusion site  
between C-terminal of P64k and P1.15

Glu Ala Asn Ala Tyr Glu  
1 5

SEQ ID NO: 10

SEQUENCE TYPE : Nucleotide

SEQUENCE LENGTH: 18 bases

MOLECULE TYPE: Sequence corresponding to the fusion of  
C-terminal from gene M-6 and from gene P1.15

GAAGCCAACG CGTACGAA

18

SEQ ID NO: 11

SEQUENCE TYPE : Amino acid

SEQUENCE LENGTH: 111 amino acids

MOLECULE TYPE: p64k N-terminal comprising homology region  
with "lypoil binding site" from E. coli Acetyl transferase

Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile Gly Gly His Glu  
1 5 10 15

Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly Asp Thr Ile  
20 25 30

Ala Val Asp Asp Thr Leu Ile Thr Leu Glu Thr Asp Lys Ala Thr  
35 40 45

Met Asp Val Pro Ala Glu Val Ala Gly Val Val Lys Glu Val Lys  
                                     50                                    55                                    60  
 5 Val Lys Val Gly Asp Lys Ile Ser Glu Gly Gly Leu Ile Val Val  
                                     65                                    70                                    75  
 Val Glu Ala Glu Gly Thr Ala Ala Ala Pro Lys Ala Glu Ser Ala  
                                     80                                    85                                    90  
 10 Ala Ala Pro Arg Lys Lys Pro Leu Lys Cys Arg Trp Val Pro Gln  
                                     95                                    100                                    105  
 Ala Ala Gln Phe Gly Gly  
 15                                    110

SEQ ID NO: 12

20 SEQUENCE TYPE : Amino acid

SEQUENCE LENGTH: 112 amino acids

MOLECULE TYPE: "lypoil binding site" from E. coli Acetyl-  
transferase

25 Val Lys Glu Val Asn Val Pro Asp Ile Gly Gly Asp Glu Val Glu  
     1                                    5                                    10                                    15  
 30 Val Thr Glu Val Met Val Lys Val Gly Asp Lys Val Ala Ala Glu  
                                     20                                    25                                    30  
 Gln Ser Leu Ile Thr Val Glu Gly Asp Lys Ala Ser Met Glu Val  
                                     35                                    40                                    45  
 35 Pro Ala Pro Phe Ala Gly Val Val Lys Glu Leu Lys Val Asn Val  
                                     50                                    55                                    60  
 Gly Asp Lys Val Lys Thr Gly Ser Leu Ile Met Ile Phe Glu Val  
                                     65                                    70                                    75  
 40 Glu Gly Ala Ala Pro Ala Ala Ala Pro Ala Lys Gln Glu Ala Ala  
                                     80                                    85                                    90  
 45 Ala Pro Ala Pro Ala Ala Lys Ala Glu Ala Pro Ala Ala Ala Pro  
                                     95                                    100                                    105  
 Ala Ala Lys Ala Glu Gly Lys  
                                     110

50

55

SEQ ID NO: 13

5

SEQUENCE TYPE : Amino acid

SEQUENCE LENGTH: 481 amino acids

10

MOLECULE TYPE: P64k fragment comprising the homology region  
with Lipoamide Dehydrogenase from E. coli

15

Ser	Ala	Asp	Ala	Glu	Tyr	Asp	Val	Val	Val	Leu	Gly	Gly	Gly	Pro
1				5					10					15

Gly	Gly	Tyr	Ser	Ala	Ala	Phe	Ala	Ala	Ala	Asp	Glu	Gly	Leu	Lys
				20					25					30

20

Val	Ala	Ile	Val	Glu	Arg	Tyr	Lys	Thr	Leu	Gly	Gly	Val	Cys	Leu
				35					40					45

Asn	Val	Gly	Cys	Ile	Pro	Ser	Lys	Ala	Leu	Leu	His	Asn	Ala	Ala
				50					55					60

25

Val	Ile	Asp	Glu	Val	Arg	His	Leu	Ala	Ala	Asn	Gly	Ile	Lys	Tyr
				65					70					75

Pro	Glu	Pro	Ala	Leu	Asp	Ile	Asp	Met	Leu	Arg	Ala	Tyr	Lys	Asp
				80					85					90

30

Gly	Val	Val	Ser	Arg	Leu	Thr	Gly	Phe	Gly	Arg	Tyr	Gly	Glu	Lys
				95					100					105

35

Arg	Lys	Val	Asp	Val	Ile	Gln	Gly	Asp	Gly	Gln	Phe	Leu	Asp	Pro
				110					115					120

His	His	Leu	Glu	Val	Ser	Leu	Thr	Ala	Gly	Asp	Ala	Tyr	Glu	Gln
				125					130					135

40

Ala	Ala	Pro	Thr	Gly	Glu	Lys	Lys	Ile	Val	Ala	Phe	Lys	Asn	Cys
				140					145					150

Ile	Ile	Ala	Ala	Gly	Ser	Arg	Val	Thr	Lys	Leu	Pro	Phe	Ile	Pro
				155					160					165

45

Glu	Asp	Pro	Arg	Ile	Ile	Asp	Ser	Ser	Gly	Ala	Leu	Ala	Leu	Lys
				170					175					180

50

Glu	Val	Pro	Gly	Lys	Leu	Leu	Ile	Ile	Gly	Gly	Gly	Ile	Ile	Gly
				185					190					195

Leu	Glu	Met	Gly	Thr	Val	Tyr	Ser	Thr	Leu	Gly	Ser	Arg	Leu	Asp
				200					205					210

55

Val	Val	Glu	Met	Met	Asp	Gly	Leu	Met	Gln	Gly	Ala	Asp	Arg	Asp
				215					220					225

5	Leu Val Lys Val	Trp Gln Lys Gln Asn Glu Tyr Arg Phe Asp Asn	230	235	240
	Ile Met Val Asn	Thr Lys Thr Val Ala Val Glu Pro Lys Glu Asp	245	250	255
10	Gly Val Tyr Val	Thr Phe Glu Gly Ala Asn Pro Pro Lys Glu Pro	260	265	270
	Gln Arg Tyr Asp	Ala Val Leu Val Ala Ala Gly Arg Ala Pro Asn	275	280	285
15	Gly Lys Leu Ile	Ser Ala Glu Lys Ala Gly Val Ala Val Thr Asp	290	295	300
	Arg Gly Phe Ile	Glu Val Asp Lys Gln Met Arg Thr Asn Val Pro	305	310	315
20	His Ile Tyr Ala	Ile Gly Asp Ile Val Gly Gln Pro Met Leu Ala	320	325	330
	His Lys Ala Val	His Glu Gly His Val Ala Ala Glu Asn Cys Ala	335	340	345
25	Gly Thr Lys Ala	Tyr Phe Asp Ala Ala Val Ile Pro Gly Val Ala	350	355	360
30	Tyr Thr Ser Pro	Glu Val Ala Trp Val Gly Glu Thr Glu Leu Ser	365	370	375
	Ala Lys Arg Pro	Ala Gly Lys Ile Thr Lys Ala Asn Phe Pro Trp	380	385	390
35	Ala Ala Ser Gly	Arg Ala Ile Ala Asn Gly Cys Asp Lys Pro Phe	395	400	405
	Thr Lys Leu Ile	Phe Asp Ala Glu Thr Gly Arg Ile Ile Gly Gly	410	415	420
40	Gly Ile Val Gly	Pro Asn Gly Gly Asp Met Ile Ala Lys Ser Ala	425	430	435
45	Leu Pro Ser Lys	Leu Gly Cys Asp Ala Ala Asp Val Gly Lys Thr	440	445	450
	Ile His Pro Arg	Pro Thr Leu Gly Glu Ser Ile Gly Met Ala Ala	455	460	465
50	Glu Val Ala Leu	Gly Thr Cys Thr Asp Leu Pro Pro Gln Lys Lys	470	475	480
55	Lys				



SEQ ID NO: 14

SEQUENCE TYPE : Amino acid

SEQUENCE LENGTH: 472 bases

MOLECULE TYPE: Segment of E. coli Lipoamide Dehydrogenase  
with homology to P64k protein

5	Ser	Thr	Glu	Ile	Lys	Thr	Gln	Val	Val	Val	Leu	Gly	Ala	Gly	Pro	1	5	10	15
15	Ala	Gly	Tyr	Ser	Ala	Ala	Phe	Arg	Cys	Ala	Asp	Leu	Gly	Leu	Glu	20	25	30	
20	Thr	Val	Ile	Val	Glu	Arg	Tyr	Asn	Thr	Leu	Gly	Gly	Val	Cys	Leu	35	40	45	
25	Asn	Val	Gly	Cys	Ile	Pro	Ser	Lys	Ala	Leu	Leu	His	Val	Ala	Lys	50	55	60	
30	Val	Ile	Glu	Glu	Ala	Lys	Ala	Leu	Ala	Glu	His	Gly	Ile	Val	Phe	65	70	75	
35	Gly	Glu	Pro	Lys	Thr	Asp	Ile	Asp	Lys	Ile	Thr	Trp	Lys	Glu	Lys	80	85	90	
40	Val	Ile	Asn	Gln	Leu	Thr	Gly	Gly	Leu	Ala	Gly	Met	Ala	Lys	Gly	95	100	105	
45	Arg	Lys	Val	Lys	Val	Val	Asn	Gly	Leu	Gly	Lys	Phe	Thr	Gly	Ala	110	115	120	
50	Asn	Thr	Leu	Glu	Val	Glu	Gly	Glu	Asn	Gly	Lys	Thr	Val	Ile	Asn	125	130	135	
55	Phe	Asp	Asn	Ala	Ile	Ile	Ala	Ala	Gly	Ser	Arg	Pro	Ile	Gln	Leu	140	145	150	
	Pro	Phe	Ile	Pro	His	Glu	Asp	Pro	Arg	Ile	Trp	Asp	Ser	Thr	Asp	155	160	165	
	Ala	Leu	Glu	Leu	Lys	Glu	Val	Pro	Glu	Arg	Leu	Leu	Val	Met	Gly	170	175	180	
	Gly	Gly	Ile	Ile	Gly	Leu	Glu	Met	Gly	Thr	Val	Tyr	His	Ala	Leu	185	190	195	
	Gly	Ser	Gln	Ile	Asp	Val	Val	Glu	Met	Phe	Asp	Gln	Val	Ile	Pro	200	205	210	
	Ala	Ala	Asp	Lys	Asp	Ile	Val	Lys	Val	Phe	Thr	Lys	Arg	Ile	Ser	215	220	225	

5	Lys Lys Phe Asn Leu Met Leu Glu Thr Lys Val Thr Ala Val Glu	230	235	240
	Ala Lys Glu Asp Gly Ile Tyr Val Thr Met Glu Gly Lys Lys Ala	245	250	255
10	Pro Ala Glu Pro Gln Arg Tyr Asp Ala Val Leu Val Ala Ile Gly	260	265	270
	Arg Val Pro Asn Gly Lys Asn Leu Asp Ala Gly Lys Ala Gly Val	275	280	285
15	Glu Val Asp Asp Arg Gly Phe Ile Arg Val Asp Lys Gln Leu Arg	290	295	300
	Thr Asn Val Pro His Ile Phe Ala Ile Gly Asp Ile Val Gly Gln	305	310	315
20	Pro Met Leu Ala His Lys Gly Val His Glu Gly His Val Ala Ala	320	325	330
	Glu Val Ile Ala Gly Lys Lys His Tyr Phe Asp Pro Lys Val Ile	335	340	345
	Pro Ser Ile Ala Tyr Thr Glu Pro Glu Val Ala Trp Val Gly Leu	350	355	360
30	Thr Glu Lys Glu Ala Lys Glu Lys Gly Ile Ser Tyr Glu Thr Ala	365	370	375
	Thr Phe Pro Trp Ala Ala Ser Gly Arg Ala Ile Ala Ser Asp Cys	380	385	390
35	Ala Asp Gly Met Thr Lys Leu Ile Phe Asp Lys Glu Ser His Arg	395	400	405
	Val Ile Gly Gly Ala Ile Val Gly Thr Asn Gly Gly Glu Leu Leu	410	415	420
	Gly Glu Ile Gly Leu Ala Ile Glu Met Gly Cys Asp Ala Glu Asp	425	430	435
45	Ile Ala Leu Thr Ile His Ala His Pro Thr Leu His Glu Ser Val	440	445	450
	Gly Leu Ala Ala Glu Val Phe Glu Gly Ser Ile Thr Asp Leu Pro	455	460	465
50	Asn Pro Lys Ala Lys Lys Lys	470		

55

**Claims**

1. A recombinant polynucleotide, comprising a nucleotide sequence coding for a protein P64k of Neisseria

meningitidis, said protein P64k essentially having the amino acid sequence shown in SEQ ID NO:1.

2. A recombinant polynucleotide according to claim 1, wherein said nucleotide sequence coding for the protein P64k of *N. meningitidis* essentially consists of the nucleotide sequence shown in SEQ ID NO:1.
3. A recombinant polynucleotide according to claim 1 or 2, further comprising a nucleotide sequence of a cloning or expression vector.
4. A transformed microorganism, containing a recombinant polynucleotide according to any of claims 1 to 3.
5. A transformed microorganism according to claim 4, which is capable of expressing the protein P64k of *N. meningitidis*.
6. A transformed microorganism according to claim 5, which is an *Escherichia coli* strain, e.g. *E. coli* strain HB101, transformed with an expression vector containing a nucleotide sequence coding for the protein P64k of *N. meningitidis*, e.g. the expression vector pM-6.
7. A recombinant proteinaceous substance, comprising an amino acid sequence corresponding to the amino acid sequence of at least a part of a protein P64k of *N. meningitidis*, said protein P64k essentially having the amino acid sequence shown in SEQ ID NO:1.
8. A recombinant proteinaceous substance according to claim 7, which is a fusion protein or a protein/polysaccharide conjugate comprising the amino acid sequence of protein P64k of *N. meningitidis*.
9. A vaccine composition, comprising a recombinant protein according to claim 7 or 8, together with a suitable carrier, diluent or adjuvant.
10. A vaccine composition, comprising a lipoamide dehydrogenase or acetyl transferase capable of inducing antibodies which can bind a protein P64k of *N. meningitidis*, together with a suitable carrier, diluent or adjuvant.
11. Monoclonal antibody, raised against a recombinant proteinaceous substance according to claim 7 or 8, or against a lipoamide dehydrogenase or acetyl transferase, and capable of binding a protein P64k of *N. meningitidis*.
12. A process for preparing a protein P64k of *Neisseria meningitidis*, or a fusion protein comprising protein P64k, said protein P64k essentially having the amino acid sequence shown in SEQ ID NO:1, comprising the steps of transforming a microorganism with an expression vector containing a nucleotide sequence coding for said protein P64k, or said fusion protein, culturing the transformed microorganism to obtain expression of said protein P64k, or said fusion protein, and isolating said expression product.
13. A method for the isolation and expression of a gene which codes for a protein belonging to the outer membrane of *N. meningitidis* and its use in vaccine preparations, wherein the gene from the strain of *N. meningitidis* B:4:P1.15, identified as M-6, is obtained from the screening of a genomic library in the EMBL 3, and is cloned and expressed in a suitable host, coding for a protein of 64kDa belonging to the outer membrane of *N. meningitidis* which has bactericidal activity against different serogroups, serotypes and subtypes of *N. meningitidis*.
14. A nucleotide sequence obtained by the method of claim 13, characterized in that the sequence is corresponding with the M-6 gene and codes for the P64k protein, identified in the sequence listing with number 1.
15. A recombinant DNA according to claims 13 and 14, characterized in that it is a molecule which contains the M-6 gene which codes for P64k protein.

16. A recombinant DNA according to claim 15, characterized in that it is a phage, a plasmid or an expression vector.
17. A recombinant DNA according to claims 15 and 16, characterized in that it is the phage EMBL 3, plasmid pM-1 and expression vector pM-6.
18. A transformed microorganism according to the preceding claims, characterized in that it results from the transformation of a suitable host, carries the M-6 gene, expresses high levels of P64k protein and maintains good viability and cellular stability.
19. A transformed microorganism according to claim 18, characterized in that it is the clone HBM64 which is obtained from the transformation of E. coli host strain HB101 with the expression vector pM-6, and it presents high stability and viability and expression levels of P64k protein higher than 25 % of the total protein of the cell.
20. A recombinant protein obtained according to the preceding claims, characterized in that it essentially has the amino acid sequence shown in the sequence listing under SEQ ID NO:1.
21. Protein P64k according to preceding claims characterized in that it is the direct result of the expression of the M-6 gene as well as any peptide which has important immunological regions obtained by chemical synthesis or enzymatic degradation of P64k protein and its use in fusion proteins and polysaccharide protein conjugates for monovalent and multivalent vaccine preparations.
22. A vaccine preparation comprising protein P64k and at least one carrier, diluent or adjuvant used for vaccine preparations, as well as comprising any protein of Lipoamide dehydrogenase or Acetyl transferase from other organism or modification thereof, which is able to induce antibodies against the P64k protein.

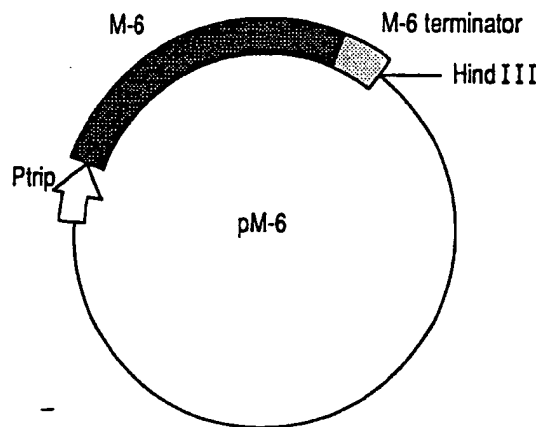


FIG. 1

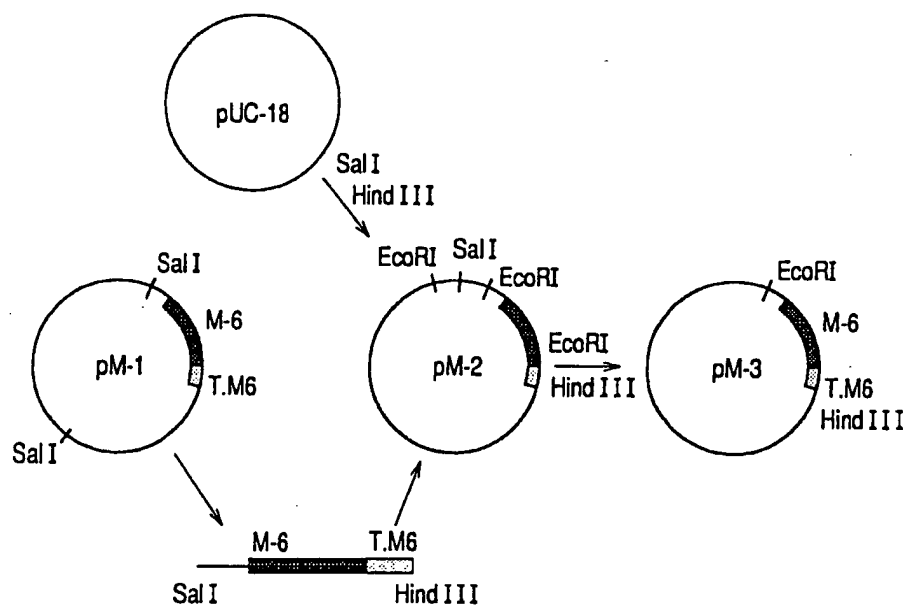
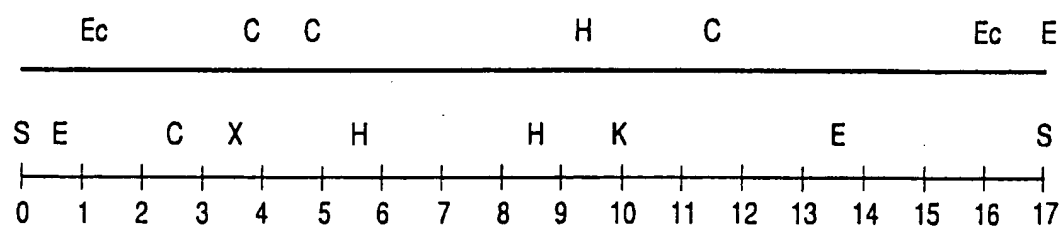


FIG. 2



S. Sal I; E. EcoRV; Ec. EcoRI; C. Cla I;  
X. Xho I; H. Hind III; K. Kpn I.

FIG. 3

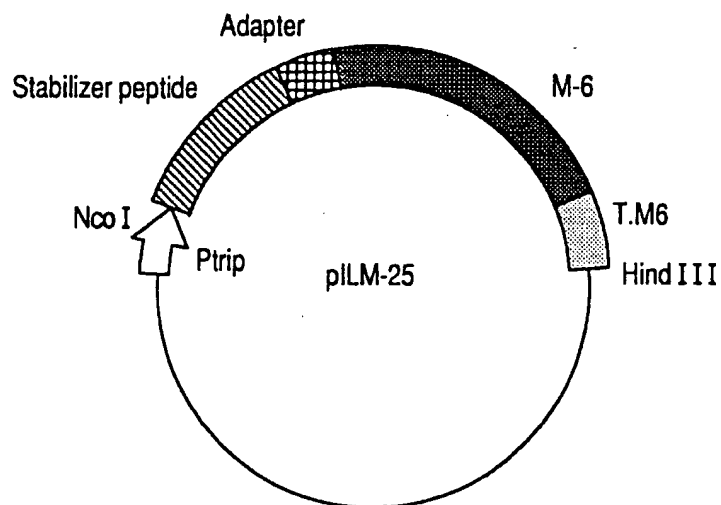


FIG. 4

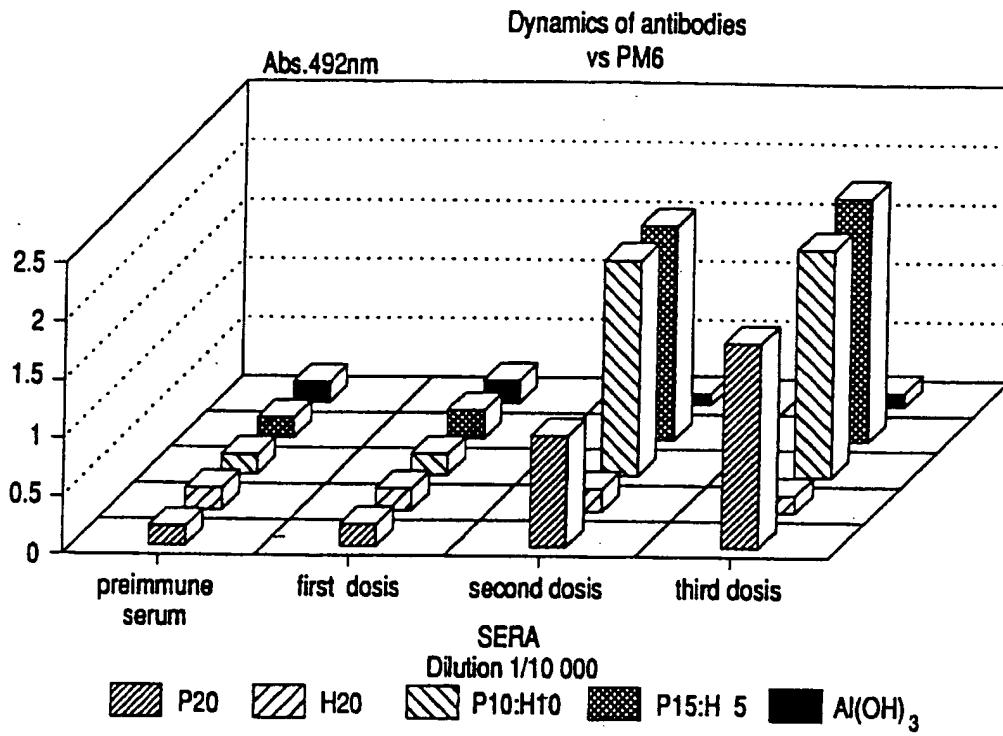


FIG. 5

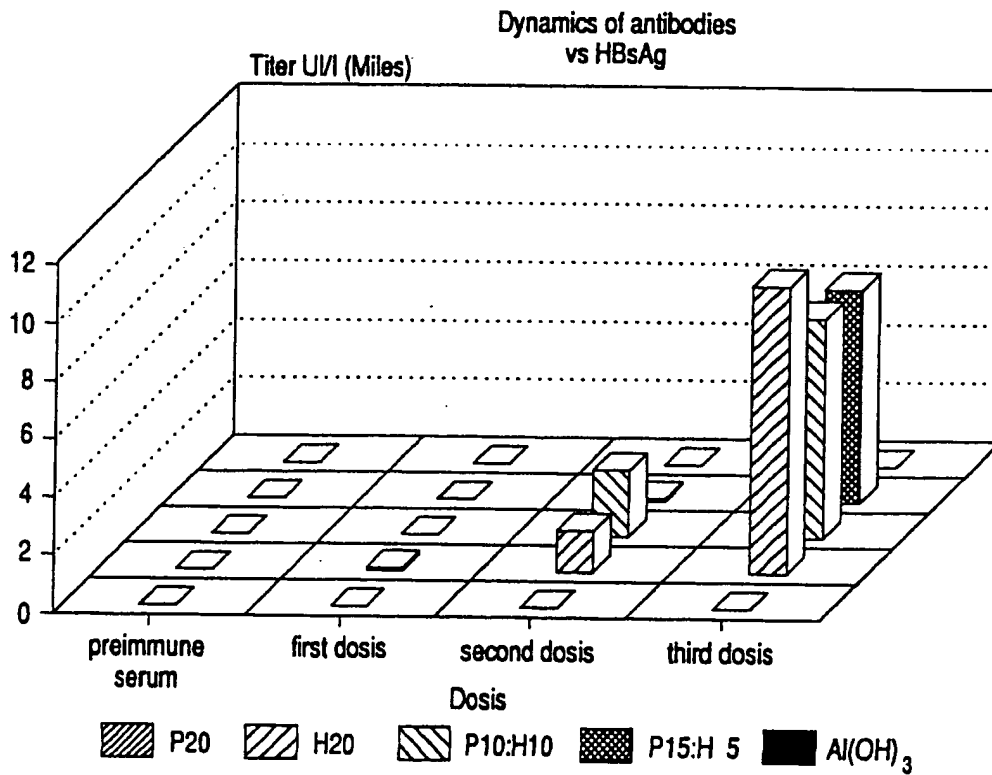


FIG. 6